

DR	PROSITE; PS00237; G_PROTEIN_REC_EP_F1_1; UNKNOWN_1.	70	LNLAISDLLEFLTFVTPFWAHYAGQWDFGNTMCFQFLTGLGYFIGFGSGIFFLILLTIDRYLA 129
KW			
Receptor	PS50262; G_PROTEIN_REC_EP_F1_2; 1.		
SEQUENCE	352 AA; 4040 MW; 3DBB43D1CC4A8687 CRC64;		
Query Match	Best Local Similarity 72.2%; Score 1371; DB 6; Length 352; Matches 258; Conservative 30; Mismatches 49; Indels 6; Gaps 2;		
Best Local Similarity 75.2%; Pred. No. 4.3e-10; Matches 258; Conservative 30; Mismatches 49; Indels 6; Gaps 2;			
Qy	24 FDYDGYA -PCKKFDVKQIGAQOLLPLPLSFLVFGFVNMLVLLINCKKLKCLTDYL 81	Qy	198 WNNFHTIMRNLLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWT 257
Db	10 YDDYDGA\$EP\$C0TQDMQHLLPLPLSFLVFGFVNMLVLLINCKRKPSMDDYL 69	Db	130 IVHAFALKARTVTPGVTTSVTLWAVFASVPGIITFLKQEDSYVCGYFPQF 189
Qy	82 LNLAISDLLEFLTLPLWAHSAANWVFGNMLVLLINCKRKPSMDDYL 141	Qy	198 WNNFHTIMRNLLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249
Db	70 LNLAISDLLEFLTLVFPWAHYAGQWDFGNTMCFQFLTGLGYFIGFGSIFILLTIDRYLA 129	Db	190 WKNFQTLKMYLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249
Qy	142 IVHAFALKARTVTPGVTTSVTLWAVFASVPGIITFLKQEDSYVCGYFPQF ---	Qy	258 PYNTVLLNTFQEFGFLSNCESTSOLIDQATOVTETLGMTHCCINP1IYAFVGEKFRYLS 317
Db	130 IVHAFALKARTVTPGVTTSVTLWAVFASVPGIITFLKQEDSYVCGYFPQF 189	Db	250 PYNTVLLNTYQEFGFLSNCNSNRDQAMQVETLGMTHCCINP1IYAFVGEKFRYLL 309
Qy	198 WNNFHTIMRNLLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWT 257	Qy	258 PYNTVLLNTFQEFGFLSNCESTSOLIDQATOVTETLGMTHCCINP1IYAFVGEKFRYLS 317
Db	190 WNFETLKMVYLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249	Db	250 PYNTVLLNTYQEFGFLSNCNSNRDQAMQVETLGMTHCCINP1IYAFVGEKFRYLL 309
Qy	258 PYNTVLLNTFQEFGFLSNCESTSOLIDQATOVTETLGMTHCCINP1IYAFVGEKFRYLS 317	Qy	318 VEFRKHTKRECKQCPVYRETVDGVTSTNTPSTGEQEVASGL 360
Db	250 PYNTVLLNTYQEFGFLSNCNSNRDQAMQVETLGMTHCCINP1IYAFVGEKFRYLL 309	Db	310 VEFQKHTAKRECKCCSIFQKEAPERANSVYTRSTGEQEVISVGL 352
Qy	318 VEFRKHTKRECKQCPVYRETVDGVTSTNTPSTGEQEVASGL 360	Qy	318 VEFRKHTKRECKQCPVYRETVDGVTSTNTPSTGEQEVASGL 360
Db	310 VEFQKHTAKRECKCCSIFQKEAPERANSVYTRSTGEQEVISVGL 352	Db	310 VEFQKHTAKRECKCCSIFQKEAPERANSVYTRSTGEQEVISVGL 352
RESULT 8		RESULT 8	
Q95NC4	PRELIMINARY; PRT: 352 AA.	Q18770	PRELIMINARY; PRT: 352 AA.
AC		ID 018770;	
DP		AC 018770;	
DR		DT 01-JAN-1998 (TREMBLrel. 05, Created)	
DR		DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DR		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DR		DE CCR5 receptor (Fragment).	
GN		GN CCR5	
OS		OS Pan troglodytes (Chimpanzee).	
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
OX		OX NCBI_TaxID=9598;	
RN		RN [1]	
RP		RP SEQUENCE FROM N_A.	
RC		RC STRAIN=MCCR5-140A;	
RA		RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.;	
RT		RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism. 4: AIDS Res. Hum. Retroviruses 0:0-0 (1997).	
RL		RL AF011538; AAB85738; 1.	
EMBL		DR InterPro: IPR000276; GPCR_Rhodopsn.	
EMBL		DR Pfam: PF00001; 7tm_1; 1.	
EMBL		DR PRINTS: PR00237; GPCR_RHODOPSN.	
EMBL		DR PROSITE: PS000237; G_PROTEIN_REC_EP_F1_1; UNKNOWN_1.	
EMBL		DR PROSITE: PS00262; G_PROTEIN_REC_EP_F1_2; 1.	
EMBL		KW Receptor.	
EMBL		FT NON_TER 352	
EMBL		SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;	
Q95NC4	SEQUENCE FROM N_A.	Q95NC4	SEQUENCE FROM N_A.
AC	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny," submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	AC	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny," submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DP	01-DEC-2001 (TREMBLrel. 19, Created)	DP	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DR	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DR	C-C chemokine receptor 5.	DR	C-C chemokine receptor 5.
GN		DR CCR5.	
OS	Atelos geoffroyi (Black-handed spider monkey).	OS Atelos geoffroyi (Black-handed spider monkey).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Atelos.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Atelos.	
OX	NCBI_TaxID=9509;	OX NCBI_TaxID=9509;	
RN	[1]	RN [1]	
RP	SEQUENCE FROM N_A.	RP	SEQUENCE FROM N_A.
RT	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny," submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	RT	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny," submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RL	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	RL	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	EMBL: AF177885; AFAK33368_1; 1.	DR	EMBL: AF177885; AFAK33368_1; 1.
DR	InterPro: IPR000276; GPCR_Rhodopsn.	DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm_1; 1.	DR	Pfam: PF00001; 7tm_1; 1.
DR	PROSITE: PS00196; G_PROTEIN_REC_EP_F1_1; UNKNOWN_1.	DR	PROSITE: PS00196; G_PROTEIN_REC_EP_F1_1; UNKNOWN_1.
DR	PROSITE: PS00237; G_PROTEIN_REC_EP_F1_2; 1.	DR	PROSITE: PS00237; G_PROTEIN_REC_EP_F1_2; 1.
DR	PROSITE: PS00262; G_PROTEIN_REC_EP_F1_2; 1.	DR	PROSITE: PS00262; G_PROTEIN_REC_EP_F1_2; 1.
KW	SEQUENCE	KW Receptor.	
SEQUENCE	352 AA; 40440 MW; FOA686CB4FE3964B CRC64;	SEQUENCE	352 AA; 40440 MW; FOA686CB4FE3964B CRC64;
Qy	24 FDYDGYA -PCKKFDVKQIGAQOLLPLPLSFLVFGFVNMLVYLILINCKKLKCLTDYL 81	Qy	24 FDYDGYA -PCKKFDVKQIGAQOLLPLPLSFLVFGFVNMLVYLILINCKKLKCLTDYL 81
Db	10 YDDYDGA\$EP\$C0TQDMQHLLPLPLSFLVFGFVNMLVYLILINCKRKPSMDDYL 69	Db	10 YDDYDGA\$EP\$C0TQDMQHLLPLPLSFLVFGFVNMLVYLILINCKRKPSMDDYL 69
Qy	82 LNLAISDLLEFLTLPLWAHSAANWVFGNAMCKLFTGLHYHIGFGGIFILLTIDRYLA 141	Qy	82 LNLAISDLLEFLTLPLWAHSAANWVFGNAMCKLFTGLHYHIGFGGIFILLTIDRYLA 141
Db	130 IVHAFALKARTVTPGVTTSVTLWAVFASVPGIITFLKQEDSYVCGYFPQF 189	Db	130 IVHAFALKARTVTPGVTTSVTLWAVFASVPGIITFLKQEDSYVCGYFPQF 189
Qy	198 WNNFHTIMRNLLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWT 257	Qy	198 WNNFHTIMRNLLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249
Db	190 WKNFQTLKMYLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249	Db	190 WKNFQTLKMYLGLVPLLINVTCYSGILKTLLCRNEKKHRRAVIFTIMVYFLFWA 249
Qy	258 PYNTVLLNTFQEFGFLSNCESTSOLIDQATOVTETLGMTHCCINP1IYAFVGEKFRYLS 317	Qy	258 PYNTVLLNTFQEFGFLSNCESTSOLIDQATOVTETLGMTHCCINP1IYAFVGEKFRYLL 309
Db	250 PYNTVLLNTYQEFGFLSNCNSNRDQAMQVETLGMTHCCINP1IYAFVGEKFRYLL 309	Db	250 PYNTVLLNTYQEFGFLSNCNSNRDQAMQVETLGMTHCCINP1IYAFVGEKFRYLL 309
Qy	318 VEFRKHTKRECKQCPVYRETVDGVTSTNTPSTGEQEVASGL 360	Qy	318 VEFRKHTKRECKQCPVYRETVDGVTSTNTPSTGEQEVASGL 360
Db	310 VEFQKHTAKRECKCCSIFQKEAPERANSVYTRSTGEQEVISVGL 352	Db	310 VEFQKHTAKRECKCCSIFQKEAPERANSVYTRSTGEQEVISVGL 352

RESULT 9									
291	IV49	Q9TV49	PRELIMINARY;	PRT;	352	AA.			
Qdy		Q9TV49							
	QAC	01-MAY-2000	(TREMBLrel.	13,	Created)				
	DDT	01-MAY-2000	(TREMBLrel.	13,	Last sequence update)				
	DDT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)				
	CC	Chemokine receptor type 5 (C-C chemokine receptor 5).							
	DE	Cercopithecus galeritus (Agile mangabey).							
	GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom							
	OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;							
	OC	Cercopithecus; Cercopithecus.							
	OC	NCBI_TaxID=532;							
	OX	[1]							
	RN	SEQUENCE FROM N.A.							
	RC	STRAIN=4;							
	RA	MEDLINE=99335215; PubMed=10408730;							
	RA	Muller-Trutwin M.C., Corbet S., Hansen J., Diop O., Georges-Courbot M.C.							
	RA	Dipp O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;							
	RA	"Mutations in CCR5-coding sequences are not associated with SIV carrier status in African nonhuman primates.";							
	RA	AIDS Res. Hum. Retroviruses 15:931-939(1999).							
	RR	[2]							
	RN	SEQUENCE FROM N.A.							
	RC	STRAIN=;							
	RA	Muller-Trutwin M.C., Corbet S., Hansen J., Diop O., Georges-Courbot M.C.							
	RA	Dipp O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;							
	RA	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.							
	RR	[3]							
	RN	SEQUENCE FROM N.A.							
	RC	Zhang Y., Ryder O.A., Zhang Y.;							
	RA	Sequence comparison of the CCR5 gene in primates and primate							
	RA	phylogeny.;							
	RA	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.							
	RR	[4]							
	RN	SEQUENCE FROM N.A.							
	RC	Zhang Y., Ryder O.A., Zhang Y.;							
	RA	Sequence comparison of the CCR5 gene in primates and primate							
	RA	phylogeny.;							
	RA	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.							
	RR	[5]							
	RN	SEQUENCE FROM N.A.							
	RC	InterPro; IPR00216; GPCR_Rhodopsn.							
	RA	PFAM; PF00001; 7tm_1; 1.							
	RA	PRINTS; PRO00237; GPCR_RHODOPSN.							
	RA	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.							
	RA	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.							
	RR	[6]							
	RN	SEQUENCE FROM N.A;							
	RC	40479 MW;							
	RA	5E1504A9B87278B2 CRC64;							
	RR	[7]							
	Q	Query Match	72.0%	Score 1368;	DB 6;	Length 352;			
	Q	Best Local Similarity	76.1%	Pred. No. 7.7e-110;					
	Q	Matches 261;	Conservative	Mismatches 45;	Indels 6;				
	Q								
	Q	24	FDYDY--GAPCHRFKDVQIGAQQLPPLYSVLFQFGVNGMVLVLLINCRKIKLCLTDI						
	Q								
	Q	10	YDIDYTSEPCQKINVQIAARLPLPVSLVLFQFGVNLIVLVLINCRKIKLKSMTDII						
	Q								
	Q	82	LNIAISDLSFLITLPLWAHSAAANNEWVGRNAMCKLFLTSLVHLYFGGFTFILITLTIDY						
	Q								
	Q	70	LNIAISDLSFLITLPLWAHSAAANNEWVGRNAMCKLFLTSLVHLYFGGFTFILITLTIDY						
	Q								
	Q	142	IYHVAFLKARIVTFGVTSVITWLVAFAVSPGIIIFTKQKEDSVIVCGYPFP---						
	Q								
	Q	130	IYHVAFLKARIVTFGVTSVITWLVAFAVSPGIIIFTKQKEDSVIVCGYPFP---						
	Q								
	Q	198	WNNFHFTIMRNLLGVLPLIMIVTCYSGILKTLRCLRNKEKRRHRAVFTFTIMIVYFLF						
	Q								
	Q	190	WKAQFQTLRIVLGVLPVLMWCYSGILKTLRCLRNKEKRRHRAVFTFTIMIVYFLF						
	Q								
	Q	258	PYNVILANTQEFFGLSNCESTSSQLDQATQVETLGTMTHCCINPITYAFGEKFRV						
	Q								
	Q	259	PNVILANTQEFFGLSNCESTSSQLDQATQVETLGTMTHCCINPITYAFGEKFRV						

Db	10	YDIDYTSECPQTKTIVNKQAAARLPLPLSUVFIGFVGNNLVLILINKRKSMTDYL	69
Dy	82	LNLASDILFLITPLWAHSANNEWFNGNAMCKFTGLYHIGHGIFIFTLITIDRYLA	141
Db	70	LNLASDILFLITPLWHAQADFGTMQCLJLGYFIGESGIFIFTLITIDRYLA	129
Dy	142	IYHAFALKARTVTFGVYTSVITWVAVASPVGIFTCKQEDSVYCCGPYFP---RG	197
Db	130	IYHAFALKARTVTFGLVTSVITWVAVASPLGIIFTYSQEGHLHYCSSHFSYQOF	189
Dy	198	WNNFHIMRNLLGHLPLLMVICSGIKTLLCRNEKKRHRVRFITIMYFLWT	257
Db	190	WKNFQPLKTVLGLVPLLYMVICSGIKTLLCRNEKKRHRVRFITIMYFLWEA	249
Dy	258	PYNIVILLNTFOEFFGLNSESTSOLIDQATQVTFGLMTHCCINPITYAVGKEFRRYLS	317
Db	250	PYNIVILLNTFOEFFGLNNSSSNRQDANQVTFGLMTHCCINPITYAVGKEFRRYLL	309
Dy	318	VFFRKHLTKRCKQCPVYRETVDGTSNTSPGEQEYASL	360
Db	310	VFFRKHLTKRCKQCSITFOOFAPEPABSSYUTRSPGEQEYASVGL	352

RESULTS 14
 2995 NC5 PRELIMINARY; PRT; 352 AA.
 Q95NC5; Q95NC5; 01-DEC-2001 (TREMBLrel. 19, Created)
 AC AC 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 C-C Chemokine receptor 5.
 CCR5.
 Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobatidae.
 NCBI_TaxID=590;
 [1]
 RN 2995 NC5
 RRP PRELIMINARY; PRT; 352 AA.
 SEQUENCE FROM N.A.
 Zhang Y., Ryder N.A., Zhang Y.;
 "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny.";
 Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 EMBL; AF177684; AAK43367.1;
 InterPro; IPR000276; GPCR_Rhodopsin.
 DRR DRR PFM00016; 7tmL1; 1.
 PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; UNKNOWN_1.
 PROSITE; PS00262; G-PROTEIN_RECPT_F1_2; 1.
 Receptor.
 KW KW 352 AA;
 SEQUENCE F4F64B3ADAF658A CRC64;
 SQ SQ 40508 MW;

